

Amendments to the Claims

This listing of claims replaces all prior versions and listings of claims in the application.

Listing of Claims

1. (Withdrawn) A gamma subunit of a vertebrate AMP-activated kinase (AMPK), wherein said gamma subunit is a polypeptide comprising at least a sequence having at least 70% identity with the polypeptide SEQ ID NO:2.
2. (Withdrawn) A polypeptide of claim 1, wherein said polypeptide comprises a sequence having at least 95% identity with the polypeptide SEQ ID NO:2.
3. (Withdrawn) A polypeptide of claim 1, wherein said polypeptide comprises a sequence having at least 75% identity with the polypeptide SEQ ID NO:28.
4. (Withdrawn) A polypeptide of claim 1, wherein said polypeptide comprises the sequence of SEQ ID NO: 2 or SEQ ID NO:4.
5. (Withdrawn) A polypeptide of claim 1, wherein said polypeptide comprises the sequence of SEQ ID NO: 28, SEQ ID NO: 30 or SEQ ID NO: 32.
6. (Withdrawn) A polypeptide which is a functionally altered mutant of a gamma subunit of a vertebrate AMP-activated kinase, wherein said polypeptide has at least a mutation located within the first CBS domain of said gamma subunit.
7. (Withdrawn) A polypeptide of claim 6, wherein the mutation is located within the region of the first CBS domain aligned with the region of a polypeptide of SEQ ID No:2 spanning from a residue 30 to residue 50.
8. (Withdrawn) A polypeptide of claim 7, wherein the mutation is a R→ Q substitution or a V→ I substitution.
9. (Withdrawn) A polypeptide of claim 8 selected from the group consisting of a polypeptide having a sequence resulting from a R→ Q substitution at a position

corresponding to position 41 of SEQ ID NO: 2;
and a polypeptide having a sequence resulting from a V→ I substitution at the position
corresponding to position 40 of SEQ ID NO: 2.

10. (Withdrawn) A polypeptide which is a mutant of a gamma subunit of a vertebrate AMP-activated kinase, wherein said polypeptide results from a deletion of a part of a polypeptide of claim 1.
11. (Currently Amended) A nucleic acid sequence encoding a polypeptide ~~of claim 1~~ comprising an amino acid sequence having at least 70% identity with the amino acid sequence set forth in SEQ ID NO:4 or SEQ ID NO:30, or the complement thereof, provided that said nucleic acid sequence does not consist of the EST GENBANK AA178898, or of the EST W94830.
12. (Currently Amended) A nucleic acid sequence of claim 11, having the sequence set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, or the complement thereof.
13. (Currently Amended) A nucleic acid sequence comprising at least a portion of a nucleic acid sequence ~~encoding a polypeptide of claim 1~~ of claim 11, and up to 500 kb of a 3' and/or of a 5' adjacent genomic DNA sequence, or the complement thereof.
14. (Currently Amended) A nucleic acid fragment selected from the group consisting of:
 - a) a specific fragment of a nucleic acid sequence encoding a gamma subunit of a vertebrate AMPK, wherein said gamma subunit is a polypeptide comprising at least a sequence having at least 70% identity with the ~~polypeptide SEQ ID NO: 2~~ sequence set forth in SEQ ID NO:4 or SEQ ID NO:30,
 - b) a specific fragment of a nucleic acid sequence encoding a polypeptide which is a functionally altered mutant of a gamma subunit of a vertebrate AMPK, wherein said polypeptide has at least a mutation located within the first CBS domain of said gamma subunit,

c) a specific fragment of a nucleic acid sequence encoding a polypeptide which is a mutant of a gamma subunit of a vertebrate AMPK, wherein said polypeptide results from a deletion of a part of a polypeptide of a) or b);
d) a nucleic acid sequence comprising at least a portion of a nucleic acid sequence encoding a polypeptide of a), b), or c), and up to 500 kb of a 3' and/or of a 5' adjacent genomic DNA sequence, or the complement thereof; and
e) a nucleic acid fragment which specifically hybridizes under stringent conditions with a nucleic acid sequence of a), b), c), or d);
provided that said nucleic acid fragment does not consist of the EST GENBANK AA178898 or of the EST GENBANK W94830.

15. (Previously Presented) A set of primers for amplifying a nucleic acid sequence, comprising a primer consisting of a nucleic acid fragment of claim 14.
16. (Currently Amended) A recombinant vector comprising a nucleic acid sequence ~~encoding a polypeptide of claim 1~~ of claim 11.
17. (Currently Amended) A host cell transformed by a nucleic acid sequence ~~encoding a polypeptide of claim 1~~ of claim 11.
18. (Withdrawn) A transgenic animal transformed by a nucleic acid sequence encoding a polypeptide of claim 1.
19. (Withdrawn) A knockout animal, wherein the gene encoding a polypeptide of claim 1 is inactive.
20. (Withdrawn) A heterotrimeric AMPK wherein the γ subunit consists of a polypeptide of claim 1.
21. (Currently Amended) A method of detecting a metabolic disorder resulting from a mutation in a gene encoding a γ subunit of AMPK, wherein said ~~process~~ method comprises:

- a) obtaining a nucleic acid sample from a vertebrate; and
b) checking for the presence in said nucleic acid of a nucleic acid sequence encoding a polypeptide ~~of claim 1~~ comprising an amino acid sequence having at least 70% identity with the amino acid sequence set forth in SEQ ID NO:4 or SEQ ID NO:30, wherein said polypeptide is functionally altered.
22. (Currently Amended) A method of claim 21 wherein the disorder is correlated with an altered glycogen accumulation in the muscular cells and results from the expression of a functionally altered allele of a polypeptide, wherein said polypeptide comprises a sequence of ~~SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:28, or SEQ ID NO:30, or SEQ ID NO:32.~~
23. (Currently Amended) A method of claim 22 wherein the presence of the nucleic acid sequence encoding said mutant polypeptide is checked by contacting said nucleic acid sample with ~~a nucleic acid~~ an oligonucleotide probe spanning said mutation, wherein said probe is complementary to a segment of said nucleic acid sequence that includes said mutation, and wherein said contacting is under conditions of specific hybridization between said probe and the mutant sequence to be detected, and detecting the hybridization complex.
- 24-25. (Canceled)
26. (Previously Presented) A method of claim 21 wherein the vertebrate is a mammal.
27. (Currently Amended) A method of claim 26, wherein said mammal is a ~~pig~~ human.
- 28-37. (Canceled)
38. (New) A nucleic acid sequence of claim 11, wherein said amino acid sequence has at least 80% identity with the amino acid sequence set forth in SEQ ID NO:4 or SEQ ID NO:30.

39. (New) A nucleic acid sequence of claim 11, wherein said amino acid sequence has at least 90% identity with the amino acid sequence set forth in SEQ ID NO:4 or SEQ ID NO:30.
40. (New) A nucleic acid fragment of claim 14, wherein the fragment is a specific fragment of a nucleic acid sequence encoding a gamma subunit of a vertebrate AMPK, wherein said gamma subunit is a polypeptide comprising at least a sequence having at least 80% identity with the sequence set forth in SEQ ID NO:4 or SEQ ID NO:30.
41. (New) A nucleic acid fragment of claim 14, wherein the fragment is a specific fragment of a nucleic acid sequence encoding a gamma subunit of a vertebrate AMPK, wherein said gamma subunit is a polypeptide comprising at least a sequence having at least 90% identity with the sequence set forth in SEQ ID NO:4 or SEQ ID NO:30.
42. (New) A method of claim 21, wherein said polypeptide comprises an amino acid sequence having at least 80% identity with the amino acid sequence set forth in SEQ ID NO:4 or SEQ ID NO:30, and wherein said polypeptide is functionally altered.
43. (New) A method of claim 21, wherein said polypeptide comprises an amino acid sequence having at least 90% identity with the amino acid sequence set forth in SEQ ID NO:4 or SEQ ID NO:30, and wherein said polypeptide is functionally altered.